SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Goodman, Corey S.

             Kidd, Thomas

             Mitchell, Kevin

             Tear, Guy

    (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and Nucleic Acids

   (iii) NUMBER OF SEQUENCES: 12

    (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

        (B) STREET: 75 DENISE DRIVE

        (C) CITY: HILLSBOROUGH

        (D) STATE: CALIFORNIA

        (E) COUNTRY: USA

        (F) ZIP: 94010

    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: Floppy disk

        (B) COMPUTER: IBM PC compatible

        (C) OPERATING SYSTEM: PC-DOS/MS-DOS

        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER:

        (B) FILING DATE:

        (C) CLASSIFICATION:

   (viii) ATTORNEY/AGENT INFORMATION:

        (A) NAME: OSMAN, RICHARD A

        (B) REGISTRATION NUMBER: 36,627

        (C) REFERENCE/DOCKET NUMBER: B98-006

    (ix) TELECOMMUNICATION INFORMATION:

        (A) TELEPHONE: (650) 343-4341

        (B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 4188 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC      60
CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCCTGCCCG CCTGGCTGCT CCTCGTCCTG     120
GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG     180
CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG     240
GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA     300
AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA     360
GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG     420
GCCGTTAGTC GCCATGCCTC CCTCCAGATA GCTGTTTTGC GCGACGATTT TCGCGTGGAG     480
CCCAAAGACA CGCGAGTGGC CAAAGGCGAG ACGGCTCTGC TGGAGTGTGG GCCGCCCAAA     540
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GCCATGTCGT TTGGCGCCAG CTCCCGCGTT CGAATTGTGG ACGGTGGCAA CCTGCTGATC     660
AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC     720
ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG     780
CCCAAGGATC AGGTGATGCT CTACGGCCAG ACAGCCACTT TCCACTGCTC AGTGGGCGGT     840
GATCCGCCGC CGAAAGTGTT GTGGAAAAAG GAGGAGGGCA ATATTCCGGT GTCCAGAGCG     900
CGAATCCTTC ACGACGAGAA AAGTTTAGAG ATATCCAACA TAACGCCCAC CGATGAGGGC     960
ACCTATGTCT GCGAGGCACA CAACAATGTC GGTCAGATCA GCGCTAGGGC TTCTCTTATA    1020
GTCCACGCTC CGCCGAACTT TACGAAAAGA CCCAGTAACA AGAAAGTGGG ACTAAATGGG    1080
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GATGGAACTC TGCAGATTAC GGATGTGCGG CAGGAAGACG AAGGCTACTA TGTGTGTTCC    1260
GCTTTCAGTG TAGTCGATTC CTCTACAGTA CGGGTTTTCC TGCAAGTCAG CTCGGTAGAC    1320
GAGCGTCCAC CTCCGATTAT TCAAATCGGA CCTGCCAATC AAACACTGCC CAAGGGATCA    1380
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GTCGATGACC TTCAACTAAG TGACTCTGGT ACCTACACCT GCACTGCATC TGGCGAACGA    1560
GGAGAAACTT CCTGGGCTGC CACACTAACG GTGGAAAAAC CCGGTTCTAC ATCTCTTCAC    1620
CGGGCAGCTG ATCCTAGCAC TTATCCTGCT CCTCCAGGAA CACCTAAAGT CCTGAATGTC    1680
AGTCGCACCA GCATTAGTCT TCGTTGGGCT AAAAGCCAAG AGAAACCCGG AGCTGTGGGC    1740
CCAATCATTG GATACACTGT AGAGTACTTC AGTCCGGATC TGCAAACTGG TTGGATTGTG    1800
GCTGCCCATC GAGTCGGCGA CACTCAAGTC ACTATCTCGG GTCTCACTCC TGGCACTTCG    1860
TATGTGTTCC TAGTTAGAGC TGAGAATACT CAGGGTATTT CTGTGCCTTC CGGCTTATCA    1920
AATGTTATTA AAACCATTGA GGCAGATTTC GATGCAGCTT CTGCCAATGA TTTGTCAGCA    1980
GCTCGAACTT TGCTGACAGG AAAGTCGGTG GAGCTAATAG ATGCCTCGGC TATCAATGCT    2040
AGTGCCGTTA GACTTGAGTG GATGCTCCAC GTGAGCGCTG ATGAGAAATA CGTAGAGGGC    2100
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CTGCGCATAC ACTATAAGGA TGCCAGTGTA CCATCCGCAC AGTATCACTC GATCACTGTT    2160

ATGGATGCCT CTGCAGAATC GTTTGTGGTG GGAAACCTTA AGAAGTACAC CAAGTATGAG    2220

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CTCACCTATG AAGATGTTCC CTCCGCACCA CCGGATAACA TTCAGATTGG CATGTACAAC    2340

CAAACAGCCG GTTGGGTGCG TTGGACTCCG CCACCCTCCC AGCACCACAA TGGCAATTTG    2400

TATGGCTACA AGATTGAGGT CAGCGCCGGT AACACCATGA AGGTGCTGGC CAATATGACT    2460

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GTGAGGTTGA ACTCCTTTAC CAAGGCAGGA GATGGACCTT ACTCCAAACC GATATCACTA    2580

TTCATGGACC CCACCCATCA TGTGCATCCG CCACGGGCAC ATCCAAGCGG CACCCATGAT    2640

GGGCGACATG AGGGACAGGA TCTCACGTAT CATAACAATG GCAACATACC ACCTGGCGAC    2700

ATTAATCCCA CCACTCATAA AAAGACCACT GACTACCTAT CTGGACCGTG GCTAATGGTG    2760

CTGGTCTGCA TCGTTCTTCT AGTCCTGGTT ATTTCGGCGG CTATTTCGAT GGTCTACTTC    2820

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ATAACCGCAT TAAATATCAA TAGCAAAGAG AGCCTTTGGA TAGACCATCA TCGTGGATGG    2940

CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT    3000

AACAGCAGTC AATCCAACTA CAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC    3060

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GCCACCACTA TGATCATTGG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA    3180

AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTGC CGGTCAGGTG    3240

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CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA    3420

AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG    3480

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CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC    3660

CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG    3720

CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG    3780

CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC    3840

CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG    3900

GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC    3960

AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG    4020

GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC    4080

TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC    4140

GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA              4188
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(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1395 amino acids.

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
1   5   10   15

Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
            20   25   30

Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
         35   40   45

Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
    50   55   60

Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
65   70   75   80

Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
            85   90   95

Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
            100   105   110

Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
         115   120   125

Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
    130   135   140

His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
145   150   155   160

Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
            165   170   175

Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
            180   185   190

Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
         195   200   205

Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
    210   215   220

Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
225   230   235   240

Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
            245   250   255

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Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
        260         265             270
Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Lys Val Leu Trp
        275             280             285
Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
        290             295             300
Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
305             310             315             320
Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
            325             330             335
Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
            340             345             350
Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
        355             360             365
Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
        370             375             380
Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
385             390             395             400
Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
            405             410             415
Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
            420             425             430
Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
        435             440             445
Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
        450             455             460
Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
465             470             475             480
Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
            485             490             495
Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
        500             505             510
Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
        515             520             525
Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
        530             535             540
Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
545             550             555             560
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Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
             565            570              575
Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
             580            585              590
Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
             595            600              605
Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
         610            615            620
Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
625              630            635                640
Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
             645            650              655
Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
             660            665              670
Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
         675            680            685
Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
         690            695            700
Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
705              710            715                720
Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
             725            730              735
Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
             740            745              750
Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
             755            760              765
Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
         770            775            780
Trp Val Arg Trp Thr Pro Pro Ser Gln His His Asn Gly Asn Leu
785              790            795                800
Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
             805            810              815
Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
             820            825              830
Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
             835            840              845
Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
         850            855            860
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Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
865   870   875   880

Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
                885   890   895

Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
            900   905   910

Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
            915   920   925

Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
    930   935   940

Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
945   950   955   960

Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
                965   970   975

His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
                980   985   990

Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
            995   1000   1005

Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
    1010   1015   1020

Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
1025   1030   1035   1040

Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Glu Thr Cys Thr Lys
            1045   1050   1055

Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
            1060   1065   1070

Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
            1075   1080   1085

Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
            1090   1095   1100

Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala
1105   1110   1115   1120

Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser
            1125   1130   1135

Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser
            1140   1145   1150

Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val
            1155   1160   1165

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Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
    1170   1175   1180

Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
1185   1190   1195   1200

Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
            1205   1210   1215

Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
            1220   1225   1230

Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
        1235   1240   1245

Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
    1250   1255   1260

Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
1265   1270   1275   1280

His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
            1285   1290   1295

Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
            1300   1305   1310

Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
        1315   1320   1325

His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
        1330   1335   1340

Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
1345   1350   1355   1360

Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
            1365   1370   1375

Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
            1380   1385   1390

Lys Asn Thr
    1395

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 4146 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

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TTTACGTTTA ATTGCCAGGC CGAGGGCAAT CCAACACCAA CCATTCAATG GTTTAAGGAC     120

GGTCGCGAAC TGAAGACGGA TACGGGTTCG CATCGCATAA TGCTGCCCGC CGGGGGTCTA     180

TTCTTTCTCA AGGTTATCCA CTCACGTAGA GAGAGCGATG CGGGCACTTA CTGGTGCGAG     240

GCCAAAAACG AGTTTGGAGT GGCACGGTCC AGGAATGCAA CGTTGCAAGT GGCAGTTCTC     300

CGCGACGAAT TCCGTTTGGA GCCGGCAAAT ACCCGCGTGG CCCAAGGCGA GGTGGCCCTG     360

ATGGAATGCG GTGCCCCCCG AGGATCTCCG GAGCCGCAAA TCTCGTGGCG CAAGAACGGC     420

CAGACCCTGA ATCTTGTCGG GAACAAGCGG ATTCGCATTG TCGACGGTGG CAATCTGGCC     480

ATCCAGGAAG CCCGCCAATC GGACGACGGA CGCTACCAGT GTGTGGTCAA GAATGTGGTT     540

GGCACCCGGG AGTCGGCCAC CGCTTTTCTT AAAGTGCATG TACGTCCATT CCTCATCCGA     600

GGACCCCAGA ATCAGACGGC GGTGGTGGGC AGCTCGGTGG TCTTCCAGTG CCGCATCGGA     660

GGCGATCCCC TGCCTGATGT CCTGTGGCGA CGCACTGCCT CCGGCGGCAA TATGCCACTG     720

CGTAAGTTTT CTTGGCTTCA TTCAGCTTCA GGTCGTGTGC ACGTACTTGA GGACCGCAGT     780

CTGAAGCTGG ACGACGTTAC TCTGGAGGAC ATGGGCGAGT ACACTTGCGA GGCGGACAAT     840

GCGGTGGGCG GCATCACGGC CACTGGCATC CTCACCGTTC ACGCTCCCCC CAAATTTGTG     900

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CCCGGCTATC GGGATGGCCG CATGGAAGTG ACCCTGACGC CCGAGGGGCG CTCGGTGCTC    1080

TCGATAGCTC GATTTGCCCG TGAGGATTCC GGAAAGGTGG TCACTTGCAA CGCCCTGAAC    1140

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TCGGATCTTC AGCGCCACGA GGATGAAGGC TTGTACACCT GCGTGGCCAG CAATCGCAAC    1440

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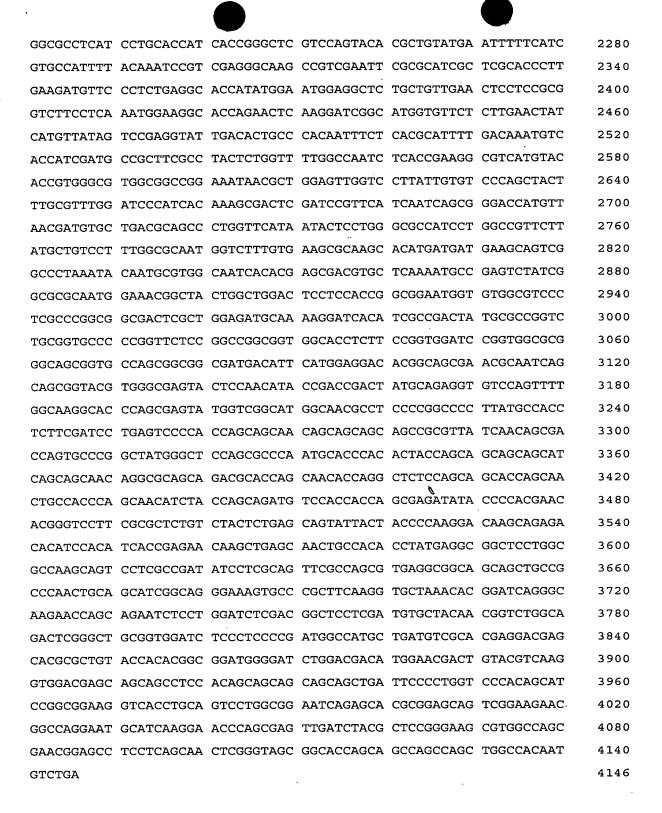
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GTGCCATTTT ACAAATCCGT CGAGGGCAAG CCGTCGAATT CGCGCATCGC TCGCACCCTT    2340
GAAGATGTTC CCTCTGAGGC ACCATATGGA ATGGAGGCTC TGCTGTTGAA CTCCTCCGCG    2400
GTCTTCCTCA AATGGAAGGC ACCAGAACTC AAGGATCGGC ATGGTGTTCT CTTGAACTAT    2460
CATGTTATAG TCCGAGGTAT TGACACTGCC CACAATTTCT CACGCATTTT GACAAATGTC    2520
ACCATCGATG CCGCTTCGCC TACTCTGGTT TTGGCCAATC TCACCGAAGG CGTCATGTAC    2580
ACCGTGGGCG TGGCGGCCGG AAATAACGCT GGAGTTGGTC CTTATTGTGT CCCAGCTACT    2640
TTGCGTTTGG ATCCCATCAC AAAGCGACTC GATCCGTTCA TCAATCAGCG GGACCATGTT    2700
AACGATGTGC TGACGCAGCC CTGGTTCATA ATACTCCTGG CGCCATCCT GGCCGTTCTT     2760
ATGCTGTCCT TTGGCGCAAT GGTCTTTGTG AAGCGCAAGC ACATGATGAT GAAGCAGTCG    2820
GCCCTAAATA CAATGCGTGG CAATCACACG AGCGACGTGC TCAAAATGCC GAGTCTATCG    2880
GCGCGCAATG GAAACGGCTA CTGGCTGGAC TCCTCCACCG GCGGAATGGT GTGGCGTCCC    2940
TCGCCCGGCG GCGACTCGCT GGAGATGCAA AAGGATCACA TCGCCGACTA TGCGCCGGTC    3000
TGCGGTGCCC CCGGTTCTCC GGCCGGCGGT GGCACCTCTT CCGGTGGATC CGGTGGCGCG    3060
GGCAGCGGTG CCAGCGGCGG CGATGACATT CATGGAGGAC ACGGCAGCGA ACGCAATCAG    3120
CAGCGGTACG TGGGCGAGTA CTCCAACATA CCGACCGACT ATGCAGAGGT GTCCAGTTTT    3180
GGCAAGGCAC CCAGCGAGTA TGGTCGGCAT GGCAACGCCT CCCCGGCCCC TTATGCCACC    3240
TCTTCGATCC TGAGTCCCCA CCAGCAGCAA CAGCAGCAGC AGCCGCGTTA TCAACAGCGA    3300
CCAGTGCCCG GCTATGGGCT CCAGCGCCCA ATGCACCCAC ACTACCAGCA GCAGCAGCAT    3360
CAGCAGCAAC AGGCGCAGCA GACGCACCAG CAACACCAGG CTCTCCAGCA GCACCAGCAA    3420
CTGCCACCCA GCAACATCTA CCAGCAGATG TCCACCACCA GCGAGATATA CCCCACGAAC    3480
ACGGGTCCTT CGCGCTCTGT CTACTCTGAG CAGTATTACT ACCCCAAGGA CAAGCAGAGA    3540
CACATCCACA TCACCGAGAA CAAGCTGAGC AACTGCCACA CCTATGAGGC GGCTCCTGGC    3600
GCCAAGCAGT CCTCGCCGAT ATCCTCGCAG TTCGCCAGCG TGAGGCGGCA GCAGCTGCCG    3660
CCCAACTGCA GCATCGGCAG GGAAAGTGCC CGCTTCAAGG TGCTAAACAC GGATCAGGGC    3720
AAGAACCAGC AGAATCTCCT GGATCTCGAC GGCTCCTCGA TGTGCTACAA CGGTCTGGCA    3780
GACTCGGGCT GCGGTGGATC TCCCTCCCCG ATGGCCATGC TGATGTCGCA CGAGGACGAG    3840
CACGCGCTGT ACCACACGGC GGATGGGGAT CTGGACGACA TGGAACGACT GTACGTCAAG    3900
GTGGACGAGC AGCAGCCTCC ACAGCAGCAG CAGCAGCTGA TTCCCCTGGT CCCACAGCAT    3960
CCGGCGGAAG GTCACCTGCA GTCCTGGCGG AATCAGAGCA CGCGGAGCAG TCGGAAGAAC.   4020
GGCCAGGAAT GCATCAAGGA ACCCAGCGAG TTGATCTACG CTCCGGGAAG CGTGGCCAGC    4080
GAACGGAGCC TCCTCAGCAA CTCGGGTAGC GGCACCAGCA GCCAGCCAGC TGGCCACAAT    4140
GTCTGA                                                              4146
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1381 amino acids

        (B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
1               5               10              15
Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
                20              25              30
Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
            35              40              45
Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
    50              55              60
Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu
65              70              75              80
Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln
                85              90              95
Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg
                100             105             110
Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly
                115             120             125
Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn
    130             135             140
Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala
145             150             155             160
Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val
                165             170             175
Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val
                180             185             190
His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val
            195             200             205
Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu
    210             215             220
Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu
225             230             235             240
Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu
            245             250             255
Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly
            260             265             270
```

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```
Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr
    275             280             285
Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys
    290             295             300
Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala
305             310             315             320
Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser
    325             330             335
Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu
    340             345             350
Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu
    355             360             365
Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser
    370             375             380
Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro
385             390             395             400
Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys
            405             410             415
Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln
            420             425             430
Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu
    435             440             445
Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln
    450             455             460
Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn
465             470             475             480
Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn
            485             490             495
Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly
            500             505             510
Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr
            515             520             525
Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly
    530             535             540
Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala
545             550             555             560
Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu
            565             570             575
```

Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
            580   585   590

Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
            595   600   605

Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
            610   615   620

Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
625   630   635   640

Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
                645   650   655

Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Ile Val Asn Asn Pro
            660   665   670

Ala Pro Val Thr Ser Asn Thr Asn Pro Leu Leu Gly Ser Thr Ser Thr
            675   680   685

Ser Ala Ser Ala Ser Ala Ser Ala Ser Ala Leu Ile Ser Thr Lys Pro
            690   695   700

Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
705   710   715   720

Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
                725   730   735

Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
                740   745   750

Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
            755   760   765

Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
            770   775   780

Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
785   790   795   800

Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
                805   810   815

Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
            820   825   830

Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
            835   840   845

Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
            850   855   860

Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
865   870   875   880

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Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln
                885   890   895

Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu
                900   905   910

Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val
                915   920   925

Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr
                930   935   940

Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser
945   950   955   960

Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met
                965   970   975

Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp
                980   985   990

His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala
                995   1000   1005

Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala
                1010   1015   1020

Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln
1025   1030   1035   1040

Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu
                1045   1050   1055

Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn
                1060   1065   1070

Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln
                1075   1080   1085

Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly
                1090   1095   1100

Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His
1105   1110   1115   1120

Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln
                1125   1130   1135

Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr
                1140   1145   1150

Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr
                1155   1160   1165

Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile
                1170   1175   1180

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```
Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly
1185                1190                1195                1200
Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg
                1205                1210                1215
Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe
                1220                1225                1230
Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp
            1235                1240                1245
Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
            1250                1255                1260
Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
1265                1270                1275                1280
His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
                1285                1290                1295
Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
                1300                1305                1310
Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
            1315                1320                1325
Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
            1330                1335                1340
Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
1345                1350                1355                1360
Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
                1365                1370                1375
Ala Gly His Asn Val
                1380
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 3894 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT    60
AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG   120
GTATCTAGGG GATCGCCAGC AACCCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC   180
```

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```
ACATGGTACA AGGATGGACA GCCCGTAATC ACGAATAAGG AGCAAGTGAA CAGCCACCGG    240
ATTGTTCTCG ACACGGGATC CCTGTTTCTT CTGAAAGTGA ATAGTGGAAA AAACGGAAAA    300
GACAGCGATG CGGGAGCGTA CTATTGTGTG GCCAGCAACG AGCACGGAGA AGTGAAGTCG    360
AACGAAGGAT CGTTAAAATT GGCGATGCTT CGCGAAGACT TTCGAGTTCG GCCAAGAACA    420
GTTCAGGCTC TTGGTGGAGA GATGGCCGTT CTGGAATGCA GTCCGCCACG TGGATTCCCG    480
GAGCCGGTTG TGAGCTGGCG GAAAGACGAC AAAGAGCTCC GAATTCAAGA CATGCCACGA    540
TACACTCTAC ACTCTGACGG AAACCTCATC ATTGATCCGG TCGATCGAAG CGATTCTGGT    600
ACTTATCAGT GTGTTGCCAA CAACATGGTC GGAGAACGGG TGTCCAATCC CGCAAGATTG    660
AGTGTCTTTG AGAAACCAAA GTTTGAGCAA GAACCCAAGG ACATGACGGT CGACGTCGGA    720
GCCGCAGTGC TGTTTGATTG TCGTGTGACT GGAGATCCTC AACCACAAAT TACGTGGAAA    780
CGCAAAAATG AGCCGATGCC AGTTACACGT GCATACATTG CCAAGGATAA TCGGGGGTTG    840
AGAATCGAAA GAGTTCAACC ATCAGACGAA GGTGAATACG TTTGCTATGC ACGAAATCCA    900
GCGGGAACTC TTGAAGCATC TGCACATCTT CGTGTCCAGG CACCTCCATC CTTCCAGACA    960
AAACCAGCAG ACCAGTCAGT TCCAGCTGGA GGCACGGCAA CTTTTGAATG CACCTTGGTC   1020
GGTCAACCGA GTCCCGCCTA TTTTTGGAGC AAGGAAGGCC AACAGGATCT TCTTTTCCCA   1080
AGTTATGTGT CCGCTGATGG TAGAACGAAA GTTTCACCAA CTGGAACATT GACAATTGAG   1140
GAAGTTCGTC AAGTTGATGA GGGAGCTTAT GTGTGCGCTG GAATGAACTC GGCAGGAAGC   1200
TCGTTGAGCA AGGCAGCTTT GAAAGCAACA TTTGAAACCA AAGGCCGTGT CCAAAAAAAA   1260
AAGAGCAAAA TGGGCAAACA GAAACAAAAA AATGTTCAAT CAATTATCAA ATATTTAATT   1320
TCAGCCGTGA CCGGAAACAC ACCCGCCAAA CCACCACCAA CAATCGAGCA TGGTCATCAA   1380
AATCAGACCC TTATGGTTGG ATCATCAGCC ATCCTTCCAT GTCAGGCTAG CGGAAAACCA   1440
ACTCCAGGAA TATCATGGCT CAGGGATGGG CTACCTATTG ACATTACAGA TAGTCGTATC   1500
AGTCAACATT CAACGGGAAG TCTACATATT GCCGATTTAA AGAAACCTGA CACCGGAGTT   1560
TACACTTGCA TTGCGAAGAA CGAGGATGGA GAGTCAACAT GGTCGGCATC TCTGACTGTT   1620
GAAGATCACA CTAGCAATGC ACAATTTGTT CGGATGCCGG ATCCATCGAA CTTCCCGTCT   1680
TCTCCAACGC AAACCCATTAT TGTCAATGTC ACTGATACCG AAGTAGAGCT CCACTGGAAT   1740
GCTCCCTCCA CATCTGGCGC AGGACCAATC ACTGGTTATA TCATTCAGTA CTACAGTCCA   1800
GACCTCGGAC AGACGTGGTT TAACATTCCA GACTACGTGG CATCTACTGA ATATAGAATA   1860
AAGGGTCTGA AACCATCTCA CTCGTATATG TTTGTGATTC GAGCAGAAAA TGAGAAAGGT   1920
ATTGGAACGC CGAGTGTGTC GTCGGCTCTC GTTACCACTA GCAAGCCAGC AGCTCAAGTT   1980
GCGCTTTCTG ACAAGAACAA AATGGACATG GCCATCGCTG AGAAGAGACT CACTTCGGAA   2040
CAACTCATAA AACTCGAGGA AGTGAAGACT ATTAATTCTA CGGCCGTTCG TTTGTTCTGG   2100
AAGAAGAGGA AACTTGAAGA GCTGATTGAT GGTTACTACA TCAAGTGGAG AGGGCCTCCA   2160
AGAACCAATG ATAATCAATA CGTGAATGTG ACCAGCCCTA GCACCGAAAA CTATGTTGTT   2220
TCAAATTTAA TGCCATTCAC CAACTATGAG TTTTTCGTGA TTCCTTATCA TTCCGGAGTT   2280
CATAGTATTC ATGGAGCACC GAGTAATTCC ATGGACGTGT TGACCGCCGA AGCTCCACCT   2340
TCATTGCCAC CAGAGGATGT GCGAATCCGT ATGCTCAACC TGACCACTCT TCGTATCTCT   2400
TGGAAAGCAC CAAAAGCCGA CGGCATCAAC GGAATTCTCA AAGGATTCCA AATTGTTATT   2460
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```
GTTGGTCAAG CGCCCAACAA CAATCGGAAC ATCACTACAA ACGAGAGAGC TGCCAGTGTT    2520

ACTCTGTTCC ATTTAGTGAC TGGAATGACG TATAAAATTC GTGTAGCGGC TAGAAGCAAT    2580

GGTGGAGTTG GAGTCTCACA TGGAACGAGT GAAGTCATCA TGAATCAAGA CACGCTGGAA    2640

AAACACCTTG CTGCTCAACA AGAAAACGAA TCATTTTTGT ATGGGCTGAT CAATAAATCT    2700

CATGTTCCTG TGATTGTCAT TGTTGCAATT CTGATTATTT TCGTAGTCAT CATTATAGCC    2760

TATTGTTACT GGAGGAATAG CAGAAACAGT GATGGAAAGG ATCGAAGTTT TATAAAGATC    2820

AATGATGGAA GTGTTCATAT GGCTTCGAAT AATCTTTGGG ATGTTGCACA AAATCCGAAT    2880

CAGAATCCAA TGTACAACAC TGCTGGAAGA ATGACTATGA ACAATAGAAA TGGCCAGGCT    2940

CTCTATTCGC TGACACCAAA TGCGCAAGAC TTTTTCAACA ATTGTGATGA CTACAGTGGA    3000

ACGATGCACA GACCAGGATC CGAGCATCAC TATCATTATG CTCAACTGAC TGGCGGACCT    3060

GGTAATGCGA TGTCTACTTT TTATGGAAAC CAATATCACG ATGATCCATC TCCATATGCC    3120

ACCACAACAC TGGTCCTGTC GAACCAACAA CCAGCTTGGC TCAATGACAA AATGCTTCGC    3180

GCGCCAGCAA TGCCAACAAA TCCCGTGCCA CCAGAGCCAC CGGCGCGATA TGCAGATCAT    3240

ACCGCTGGAA GACGATCTCG ATCGAGCCGT GCATCCGATG GGAGAGGAAC TCTGAATGGC    3300

GGACTCCATC ACCGGACTAG CGGAAGTCAA CGGTCGGATA GTCCACCTCA CACAGATGTG    3360

AGCTATGTTC AGCTTCACTC ATCCGATGGA ACTGGTAGTA GTAAGGAAAG AACTGGGGAG    3420

CGGAGAACAC CACCGAATAA GACTCTGATG GACTTTATTC CGCCACCACC TTCCAATCCA    3480

CCACCACCTG GAGGGCACGT TTATGACACA GCAACTAGGC GTCAGTTGAA TCGTGGAAGT    3540

ACTCCACGAG AAGACACCTA CGATTCGGTC AGTGACGGAG CTTTTGCTCG GGTTGATGTG    3600

AATGCAAGGC CAACGAGTCG GAATCGGAAT TTGGGAGGAA GGCCGCTGAA AGGGAAACGA    3660

GACGACGATA GTCAGCGGTC TTCGTTGATG ATGGACGATG ATGGTGGATC TTCTGAAGCT    3720

GACGGGGAGA ACTCTGAAGG AGACGTTCCG CGTGGAGGTG TTAGAAAAGC AGTTCCTCGA    3780

ATGGGTATCT CTGCAAGTAC GCTGGCTCAT AGTTGTTACG GGACAAACGG CACTGCTCAA    3840

CGATTCCGGT CAATTCCACG TAACAATGGA ATCGTCACAC AAGAACAAAC TTGA          3894
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1297 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Tyr Tyr Leu Gly Phe Tyr His Thr His Thr His Thr His Thr Tyr
1               5                   10                  15

Ile Asn Phe Asp Lys Ile Pro Asn Ala Ser Asn Leu Ala Pro Val Ile
                20                  25                  30

Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr
```

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```
          35                      40                      45
Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys
          50                      55                      60
Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg
65                      70                      75                      80
Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly
                    85                      90                      95
Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser
                    100                     105                     110
Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala
                    115                     120                     125
Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu
          130                     135                     140
Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe Pro
145                     150                     155                     160
Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile Gln
                    165                     170                     175
Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile Asp
                    180                     185                     190
Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn Asn
                    195                     200                     205
Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe Glu
          210                     215                     220
Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val Gly
225                     230                     235                     240
Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro Gln
                    245                     250                     255
Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala Tyr
                    260                     265                     270
Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro Ser
                    275                     280                     285
Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr Leu
          290                     295                     300
Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln Thr
305                     310                     315                     320
Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe Glu
                    325                     330                     335
Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys Glu
```

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Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly Arg
                355   360   365
Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg Gln
                370   375   380
Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly Ser
385   390   395   400
Ser Leu Ser Lys Ala Ala Leu Lys Ala Thr Phe Glu Thr Lys Gly Arg
                405   410   415
Val Gln Lys Lys Lys Ser Lys Met Gly Lys Gln Lys Gln Lys Asn Val
                420   425   430
Gln Ser Ile Ile Lys Tyr Leu Ile Ser Ala Val Thr Gly Asn Thr Pro
                435   440   445
Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln Asn Gln Thr Leu
                450   455   460
Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala Ser Gly Lys Pro
465   470   475   480
Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro Ile Asp Ile Thr
                485   490   495
Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu His Ile Ala Asp
                500   505   510
Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile Ala Lys Asn Glu
                515   520   525
Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val Glu Asp His Thr
                530   535   540
Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser Asn Phe Pro Ser
545   550   555   560
Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp Thr Glu Val Glu
                565   570   575
Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly Pro Ile Thr Gly
                580   585   590
Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln Thr Trp Phe Asn
                595   600   605
Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile Lys Gly Leu Lys
                610   615   620
Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu Asn Glu Lys Gly
625   630   635   640
Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr Thr Ser Lys Pro

```
                       645                     650                     655
Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met Asp Met Ala Ile
              660                     665                     670
Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys Leu Glu Glu Val
              675                     680                     685
Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp Lys Lys Arg Lys
      690                     695                     700
Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp Arg Gly Pro Pro
705                     710                     715                     720
Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser Pro Ser Thr Glu
              725                     730                     735
Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn Tyr Glu Phe Phe
              740                     745                     750
Val Ile Pro Tyr His Ser Gly Val His Ser Ile His Gly Ala Pro Ser
      755                     760                     765
Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro
      770                     775                     780
Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr Leu Arg Ile Ser
785                     790                     795                     800
Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile Leu Lys Gly Phe
              805                     810                     815
Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn Arg Asn Ile Thr
              820                     825                     830
Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His Leu Val Thr Gly
      835                     840                     845
Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn Gly Gly Val Gly
      850                     855                     860
Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln Asp Thr Leu Glu
865                     870                     875                     880
Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe Leu Tyr Gly Leu
              885                     890                     895
Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val Ala Ile Leu Ile
              900                     905                     910
Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp Arg Asn Ser Arg
      915                     920                     925
Asn Ser Asp Gly Lys Asp Arg Ser Phe Ile Lys Ile Asn Asp Gly Ser
      930                     935                     940
Val His Met Ala Ser Asn Asn Leu Trp Asp Val Ala Gln Asn Pro Asn
```

945   950   955   960
Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg
                965   970   975
Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe
                980   985   990
Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu
                995   1000   1005
His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met
        1010   1015   1020
Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala
1025   1030   1035   1040
Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp
                1045   1050   1055
Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu
                1060   1065   1070
Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser
                1075   1080   1085
Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His
                1090   1095   1100
Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val
1105   1110   1115   1120
Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu
                1125   1130   1135
Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe
                1140   1145   1150
Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Gly Gly His Val Tyr
                1155   1160   1165
Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu
                1170   1175   1180
Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val
1185   1190   1195   1200
Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu
                1205   1210   1215
Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp
                1220   1225   1230
Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp
        1235   1240   1245
Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser

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```
        1250              1255              1260
     Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln
     1265              1270              1275              1280
     Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln
              1285              1290              1295
     Thr
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 4956 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT      60
CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC     120
GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT     180
CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA     240
AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA     300
TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG     360
TTGCTGCCGA GTGGATCTTT ATTTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT     420
GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG AGAGGCTGT GAGCCACAAT     480
GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG     540
GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC     600
ACCATTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AAGATGAAAG AATAACTATA     660
CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT     720
GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG     780
AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA     840
TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA     900
GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG     960
ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA    1020
GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG    1080
GTTGTTGCTT TGGGACGGAC TGTAACTTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA    1140
GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG    1200
TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA    1260
TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG    1320
GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT    1380
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CCTGTGAATC AGACTGTAGC CGTGGATGGC ACTTTCGTCC TCAGCTGTGT GGCCACAGGC    1440
AGTCCAGTGC CCACCATTCT GTGGAGAAAG GATGGAGTCC TCGTTTCAAC CCAAGACTCT    1500
CGAATCAAAC AGTTGGAGAA TGGAGTACTG CAGATCCGAT ATGCTAAGCT GGGTGATACT    1560
GGTCGGTACA CCTGCATTGC ATCAACCCCC AGTGGTGAAG CAACATGGAG TGCTTACATT    1620
GAAGTTCAAG AATTTGGAGT TCCAGTTCAG CCTCCAAGAC CTACTGACCC AAATTTAATC    1680
CCTAGTGCCC CATCAAAACC TGAAGTGACA GATGTCAGCA GAAATACAGT CACATTATCG    1740
TGGCAACCAA ATTTGAATTC AGGAGCAACT CCAACATCTT ATATTATAGA AGCCTTCAGC    1800
CATGCATCTG GTAGCAGCTG GCAGACCGTA GCAGAGAATG TGAAAACAGA AACATCTGCC    1860
ATTAAAGGAC TCAAACCTAA TGCAATTTAC CTTTTCCTTG TGAGGGCAGC TAATGCATAT    1920
GGAATTAGTG ATCCAAGCCA AATATCAGAT CCAGTGAAAA CACAAGATGT CCTACCAACA    1980
AGTCAGGGGG TGGACCACAA GCAGGTCCAG AGAGAGCTGG GAAATGCTGT TCTGCACCTC    2040
CACAACCCCA CCGTCCTTTC TTCCTCTTCC ATCGAAGTGC ACTGGACAGT AGATCAACAG    2100
TCTCAGTATA TACAAGGATA TAAAATTCTC TATCGGCCAT CTGGAGCCAA CCACGGAGAA    2160
TCAGACTGGT TAGTTTTTGA AGTGAGGACG CCAGCCAAAA ACAGTGTGGT AATCCCTGAT    2220
CTCAGAAAGG GAGTCAACTA TGAAATTAAG GCTCGCCCTT TTTTTAATGA ATTTCAAGGA    2280
GCAGATAGTG AAATCAAGTT TGCCAAAACC CTGGAAGAAG CACCCAGTGC CCCACCCCAA    2340
GGTGTAACTG TATCCAAGAA TGATGGAAAC GGAACTGCAA TTCTAGTTAG TTGGCAGCCA    2400
CCTCCAGAAG ACACTCAAAA TGGAATGGTC CAAGAGTATA AGGTTTGGTG TCTGGGCAAT    2460
GAAACTCGAT ACCACATCAA CAAAACAGTG GATGGTTCCA CCTTTTCCGT GGTCATTCCC    2520
TTTCTTGTTC CTGGAATCCG ATACAGTGTG GAAGTGGCAG CCAGCACTGG GGCTGGGTCT    2580
GGGGTAAAGA GTGAGCCTCA GTTCATCCAG CTGGATGCCC ATGGAAACCC TGTGTCACCT    2640
GAGGACCAAG TCAGCCTCGC TCAGCAGATT TCAGATGTGG TGAAGCAGCC GGCCTTCATA    2700
GCAGGTATTG GAGCAGCCTG TTGGATCATC CTCATGGTCT TCAGCATCTG GCTTTATCGA    2760
CACCGCAAGA AGAGAAACGG ACTTACTAGT ACCTACGCGG GTATCAGAAA AGTCCCGTCT    2820
TTTACCTTCA CACCAACAGT AACTTACCAG AGAGGAGGCG AAGCTGTCAG CAGTGGAGGG    2880
AGGCCTGGAC TTCTCAACAT CAGTGAACCT GCCGCGCAGC CATGGCTGGC AGACACGTGG    2940
CCTAATACTG GCAACAACCA CAATGACTGC TCCATCAGCT GCTGCACGGC AGGCAATGGA    3000
AACAGCGACA GCAACCTCAC TACCTACAGT CGCCCAGCTG ATTGTATAGC AAATTATAAC    3060
AACCAACTGG ATAACAAACA AACAAATCTG ATGCTCCCTG AGTCAACTGT TTATGGTGAT    3120
GTGGACCTTA GTAACAAAAT CAATGAGATG AAAACCTTCA ATAGCCCAAA TCTGAAGGAT    3180
GGGCGTTTTG TCAATCCATC AGGGCAGCCT ACTCCTTACG CCACCACTCA GCTCATCCAG    3240
TCAAACCTCA GCAACAACAT GAACAATGGC AGCGGGGACT CTGGCGAGAA GCACTGGAAA    3300
CCACTGGGAC AGCAGAAACA AGAAGTGGCA CCAGTTCAGT ACAACATCGT GGAGCAAAAC    3360
AAGCTGAACA AAGATTATCG AGCAAATGAC ACAGTTCCTC CAACTATCCC ATACAACCAA    3420
TCATACGACC AGAACACAGG AGGATCCTAC AACAGCTCAG ACCGGGGCAG TAGTACATCT    3480
GGGAGTCAGG GGCACAAGAA AGGGGCAAGA ACACCCAAGG TACCAAAACA GGGTGGCATG    3540
AACTGGGCAG ACCTGCTTCC TCCTCCCCCA GCACATCCTC CTCCACACAG CAATAGCGAA    3600
GAGTACAACA TTTCTGTAGA TGAAAGCTAT GACCAAGAAA TGCCATGTCC CGTGCCACCA    3660
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GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT    3720

CCCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT    3780

GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG    3840

GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA    3900

CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTTCAGGACC CCTGGTCTCA    3960

GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG    4020

ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTTGGG    4080

GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG    4140

GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCACTGAT    4200

GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA    4260

CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC    4320

ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA    4380

GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT    4440

CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCAATC CAAGACACAG    4500

CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA    4560

TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT    4620

GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG    4680

AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC    4740

CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT    4800

                                                          Leu  Ser
CCCAGTTCCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA    4860

AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTACTTG GAGGATATGA AAGAGGAGAA    4920

GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA                              4956
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1651 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
1               5                   10                  15

Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
            20                  25                  30

Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
        35                  40                  45

Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu
```

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```
              50                      55                      60
Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser
65                      70                      75                      80
Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr
              85                      90                      95
Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys
              100                     105                     110
Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe
              115                     120                     125
Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val
              130                     135                     140
Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn
145                     150                     155                     160
Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro
              165                     170                     175
Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln
              180                     185                     190
Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly
              195                     200                     205
Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys
              210                     215                     220
Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys
225                     230                     235                     240
Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu
              245                     250                     255
Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala
              260                     265                     270
Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp
              275                     280                     285
Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys
              290                     295                     300
Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val
305                     310                     315                     320
Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val
              325                     330                     335
Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His
              340                     345                     350
Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val
```

```
                 355                    360                    365
Thr Phe Gln Cys Glu Ala Thr Gly Asn Pro Gln Pro Ala Ile Phe Trp
         370                    375                    380
Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr Gln Pro Pro Gln
385                    390                    395                    400
Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp Leu Thr Ile Thr
                     405                    410                    415
Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys Gln Thr Leu Asn
                 420                    425                    430
Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu Val Thr Asp Val
             435                    440                    445
Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly Pro Val Asn Gln
         450                    455                    460
Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys Val Ala Thr Gly
465                    470                    475                    480
Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly Val Leu Val Ser
                     485                    490                    495
Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly Val Leu Gln Ile
                 500                    505                    510
Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr Cys Ile Ala Ser
             515                    520                    525
Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile Glu Val Gln Glu
         530                    535                    540
Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile
545                    550                    555                    560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr
                     565                    570                    575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr
                 580                    585                    590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln
                 595                    600                    605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu
         610                    615                    620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr
625                    630                    635                    640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp
                     645                    650                    655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu
```

```
                660                    665                    670
Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser
        675                    680                    685
Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile
        690                    695     ,              700
Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu
705                    710                    715                    720
Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val
                725                    730                    735
Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg
                740                    745                    750
Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala
                755                    760                    765
Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val
        770                    775                    780
Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro
785                    790                    795                    800
Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp
                805                    810                    815
Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly
                820                    825                    830
Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr
        835                    840                    845
Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser
        850                    855                    860
Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn Pro Val Ser Pro
865                    870                    875                    880
Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp Val Val Lys Gln
                885                    890                    895
Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp Ile Ile Leu Met
                900                    905                    910
Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys Arg Asn Gly Leu
        915                    920                    925
Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Pro Ser Phe Thr Phe Thr
        930                    935                    940
Pro Thr Val Thr Tyr Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly
945                    950                    955                    960
Arg Pro Gly Leu Leu Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu
```

Ala Asp Thr Trp Pro Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile

              980   985   990

Ser Cys Cys Thr Ala Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr

              995   1000   1005

Tyr Ser Arg Pro Ala Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp

        1010   1015   1020

Asn Lys Gln Thr Asn Leu Met Leu Pro Glu Ser Thr Val Tyr Gly Asp

1025   1030   1035   1040

Val Asp Leu Ser Asn Lys Ile Asn Glu Met Lys Thr Phe Asn Ser Pro

              1045   1050   1055

Asn Leu Lys Asp Gly Arg Phe Val Asn Pro Ser Gly Gln Pro Thr Pro

              1060   1065   1070

Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn Leu Ser Asn Asn Met Asn

              1075   1080   1085

Asn Gly Ser Gly Asp Ser Gly Glu Lys His Trp Lys Pro Leu Gly Gln

        1090   1095   1100

Gln Lys Gln Glu Val Ala Pro Val Gln Tyr Asn Ile Val Glu Gln Asn

1105   1110   1115   1120

Lys Leu Asn Lys Asp Tyr Arg Ala Asn Asp Thr Val Pro Pro Thr Ile

              1125   1130   1135

Pro Tyr Asn Gln Ser Tyr Asp Gln Asn Thr Gly Gly Ser Tyr Asn Ser

              1140   1145   1150

Ser Asp Arg Gly Ser Ser Thr Ser Gly Ser Gln Gly His Lys Lys Gly

        1155   1160   1165

Ala Arg Thr Pro Lys Val Pro Lys Gln Gly Gly Met Asn Trp Ala Asp

        1170   1175   1180

Leu Leu Pro Pro Pro Pro Ala His Pro Pro His Ser Asn Ser Glu

1185   1190   1195   1200

Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys

              1205   1210   1215

Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu

              1220   1225   1230

Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser

        1235   1240   1245

Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr

        1250   1255   1260

Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu

Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val

1285   1290   1295

Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly

1300   1305   1310

Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu

1315   1320   1325

Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg

1330   1335   1340

Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly

1345   1350   1355   1360

Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser

1365   1370   1375

Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser

1380   1385   1390

Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala

1395   1400   1405

Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln

1410   1415   1420

Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro

1425   1430   1435   1440

Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln

1445   1450   1455

Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg

1460   1465   1470

Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Val Pro Pro Pro

1475   1480   1485

Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg

1490   1495   1500

Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg

1505   1510   1515   1520

Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp

1525   1530   1535

Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu

1540   1545   1550

Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala

1555   1560   1565

Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile

```
1570              1575              1580
```

Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp

```
1585              1590              1595              1600
```

Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln

```
        1605              1610              1615
```

Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val

```
        1620              1625              1630
```

Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu

```
        1635              1640              1645
```

Thr Glu Ser

```
        1650
```


(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1300 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:

        (A) NAME/KEY: misc_feature

        (B) LOCATION: 855..1187

        (D) OTHER INFORMATION: /note= "N signifies gap in sequence"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAACTAAAGG AAACCCACAG      60
CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAAA CCAACCCCAG     120
CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA     180
CGTTCCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA     240
AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA     300
GGCCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT     360
GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT     420
CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTTCTGAT     480
ACTGGCACTT ATACTTGTGT GGCTACAAGT TCAAGTGGAG AGGCTTCCTG GAGTGCAGTG     540
CTGGATGTGA CAGAGTCTGG AGCAACAATC AGTAAAAACT ATGATTTAAG TGACCTGCCA     600
GGGCCACCAT CCAAACCGCA AGTCACTGAT GTTACTAAGA ACAGTGTCAC CTTGTCCTGG     660
CAGCCAGGTA CCCCTGGAAC CCTTCCAGCA AGTGCATATA TCATTGAGGC TTTCAGCCAA     720
TCAGTGAGCA ACAGCTGGCA GACCGTGGCA AACCATGTAA AGACCACCCT CTATACTGTA     780
AGAGGACTGC GGCCCAATAC AATCTACTTA TTCATGGTCA GAGCGATCAA CCCCAAGGTY     840
```

```
TCAGTGACCC AAGTNAAACC ACAGAAAAAC AATGGATCCA CTTGGGCCAA TGTCCCTCTA      900

CCTCCCCCCC CAGTCCAGCC CCTTCCTGGC ACGGAGCTGG AACACTATGC AGTGGAACAA      960

CAAGAAAATG GCTATGACAG TGATAGCTGG TGCCCACCAT TGCCAGTACA AACTTACTTA     1020

CACCAAGGTC TGGAAGATGA ACTGGAAGAA GATGATGATA GGGTCCCAAC ACCTCCTGTT     1080

CGAGGCGTGG CTTCTTCTCC TGCTATCTCC TTTGGACAGC AGTCCACTGC AACTCTTACT     1140

CCATCCCCAC GGGAAGAGAT GCAACCCATG CTGCAGGCTT CACCTNTTTA CCTCCTCTCA     1200

AAGACCTCGA CCTACCAGCC CATTTTCTAC TGACAGTAAC ACCAGTGCAG CCCTGAGTCA     1260

AAGTCAGAGG CCTCGGCCCA CTAAAAAACA CAAGGGAGGG                          1300
```

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 434 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (A) NAME/KEY: Modified-site

        (B) LOCATION: 285..396

        (D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Gln Ile Val Ala Gln Gly Arg Thr Val Thr Phe Pro Cys Glu Thr Lys
1               5                   10                  15

Gly Asn Pro Gln Pro Ala Val Phe Trp Gln Lys Glu Gly Ser Gln Asn
                20                  25                  30

Leu Leu Phe Pro Asn Gln Pro Gln Pro Asn Ser Arg Cys Ser Val
            35                  40                  45

Ser Pro Thr Gly Asp Leu Thr Ile Thr Asn Ile Gln Arg Ser Asp Ala
        50                  55                  60

Gly Tyr Tyr Ile Cys Gln Ala Leu Thr Val Ala Gly Ser Ile Leu Ala
65                  70                  75                  80

Lys Ala Gln Leu Glu Val Thr Asp Val Leu Thr Asp Arg Pro Pro Pro
                85                  90                  95

Ile Ile Leu Gln Gly Pro Ala Asn Gln Thr Leu Ala Val Asp Gly Thr
                100                 105                 110

Ala Leu Leu Lys Cys Lys Ala Thr Gly Asp Pro Leu Pro Val Ile Ser
        115                 120                 125

Trp Leu Lys Glu Gly Phe Thr Phe Pro Gly Arg Asp Pro Arg Ala Thr
```

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Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys Asn Leu Arg Ile Ser Asp

145   150   155   160

Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser Ser Ser Gly Glu Ala Ser

                        165   170   175

Trp Ser Ala Val Leu Asp Val Thr Glu Ser Gly Ala Thr Ile Ser Lys

                        180   185   190

Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro Ser Lys Pro Gln Val

                        195   200   205

Thr Asp Val Thr Lys Asn Ser Val Thr Leu Ser Trp Gln Pro Gly Thr

                        210   215   220

Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln

225   230   235   240

Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr

                        245   250   255

Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met

                        260   265   270

Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln

                        275   280   285

Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro

                        290   295   300

Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln

305   310   315   320

Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val

                        325   330   335

Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp

                        340   345   350

Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala

                        355   360   365

Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg

                        370   375   380

Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser

385   390   395   400

Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser

                        405   410   415

Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys

                        420   425   430

Gly Gly

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 444 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GCCCAGGCAG TTGCTGCAGC TGCGGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG      60

CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT     120

GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG     180

CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCCT     240

CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA     300

CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC     360

AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG     420

CGAACAAATC CAAGTGACCC CAGA                                           444
```

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 148 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala
1               5                   10                  15

Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser
            20                  25                  30

Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser
            35                  40                  45

Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln
    50                  55                  60

Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro
65                  70                  75                  80

Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala
                85                  90                  95
```

Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu
        100   105   110
Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly
        115   120   125
Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro
        130   135   140
Ser Asp Pro Arg
145